

A¹

at portions where binding sites are sparse, the microstructures are physically remote from one another and yet functional, or they are functionally independent from one another.

Please add new Claim 6 as follows:

A²

6. (New) The method for predicting the structure of a gene regulator binding site as described in claim 2, wherein, from the searched parameter sets, microstructures comprising binding sites of the enhancer or promoter, some of the binding sites interacting locally with one another, are predicted as follows:

at portions where binding sites are dense, the microstructures are physically close to one another for interaction therebetween, or they are physically remote from one another but interact with one another closely and functionally, and

at portions where binding sites are sparse, the microstructures are physically remote from one another and yet functional, or they are functionally independent from one another.

IN THE ABSTRACT

Please amend the Abstract on page 31 as follows:

ABSTRACT

A³

A method for predicting the structure of a binding site to which a gene regulator binds, which method enables, through investigation of the internal structure of an enhancer or promoter, transcriptional regulation of a gene to be more clearly elucidated. The method provides a gene of interest, of which a user of the method desires to predict regulation-related structures of binding sites to which regulators bind, the binding sites being present within an enhancer or promoter region to which a protein serving as a transcriptional element is bound and which is present upstream or downstream to a coding region of the gene. A calculation model for each of the binding sites is constructed within the enhancer or promoter region, the